EC 3.3.2.6

Common name: leukotriene-A_4 hydrolase

Reaction: (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicosa-7,9,11,14-tetraenoate + H_2O = (6Z,8E,10E,14Z)-(5S,12R)-5,12-dihydroxyicosa-6,8,10,14-tetraenoate

Other name(s): LTA$_4$ hydrolase; LTA4H

Systematic name: (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicosa-7,9,11,14-tetraenoate hydrolase

Comments: Converts 4,5-leukotriene A_4 into leukotriene B_4. Highly specific. Not identical with EC 3.3.2.3 epoxide hydrolase.

Links to other databases: BRENDA, EXPASY, KEGG, ERGO, PDB, CAS registry number: 90119-07-6

References:

1. Evans, J.F., Dupuis, P. and Ford-Hutchinson, A.W. Purification and characterisation of leukotriene A_4 hydrolase from rat neutrophils. *Biochim. Biophys. Acta* 840 (1985) 43-50. [Medline UI: 85200023]

2. Minami, M., Ohno, S., Kawasaki, H., Rådmark, O., Samuelsson, B., Jörnvall, H., Shimizu, T., Seyama, Y. and Suzuki, K. Molecular cloning of a cDNA coding for human leukotriene A_4 hydrolase - complete primary structure of an enzyme involved in eicosanoid synthesis. *J. Biol. Chem.* 262 (1987) 13873-13876.

[EC 3.3.2.6 created 1989]

Return to EC 3.3.2 home page
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☑ **1HS6**   **STRUCTURE OF LEUKOTRIENE A4 HYDROLASE COMPLEXED WITH BESTATIN.**

Chains	A
E Value	0.0
Characteristics	Deposited: 24-Dec-2000 Exp. Method: X Ray Diffraction Resolution: 1.95 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase
Authors	Thunnissen, M.M., Nordlund, P., Haeggstrom, J.Z.
Alignment stats	Length: 610 Score: 1222.99bits (3163) E-value: 0.0 Identities: 610/610 (100%) Positives: 610/61 (100%) Gaps: 0/610 (0%)

Alignment
```
           1        10        20        30        40        50        60
           |         |         |         |         |         |         |
Query PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
      PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
Sbjct PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
           |         |         |         |         |         |         |
           2        10        20        30        40        50        60
```

☑ **1H19**   **STRUCTURE OF [E271Q] LEUKOTRIENE A4 HYDROLASE**

Chains	A
E Value	0.0
Characteristics	Deposited: 04-Jul-2002 Exp. Method: X Ray Diffraction Resolution: 2.10 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: YES
Authors	Rudberg, P.C., Tholander, F., Thunnissen, M.M., Haeggstrom, J.Z.
Alignment stats	Length: 610 Score: 1221.84bits (3160) E-value: 0.0 Identities: 609/610 (100%) Positives: 610/61 (100%) Gaps: 0/610 (0%)

Alignment
```
           1        10        20        30        40        50        60
           |         |         |         |         |         |         |
Query PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
      PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
Sbjct PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
           |         |         |         |         |         |         |
           2        10        20        30        40        50        60
```

☑ **1GW6**   **STRUCTURE OF LEUKOTRIENE A4 HYDROLASE D375N MUTANT**

Chains	A
E Value	0.0
Characteristics	Deposited: 07-Mar-2002 Exp. Method: X Ray Diffraction Resolution: 2.20 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: YES
Authors	Rudberg, P., Tholander, F., Thunnissen, M., Samuelsson, B., Haeggstrom, J.
Alignment stats	Length: 610 Score: 1221.07bits (3158) E-value: 0.0 Identities: 609/610 (100%) Positives: 610/61 (100%) Gaps: 0/610 (0%)

Alignment
```
           1        10        20        30        40        50        60
           |         |         |         |         |         |         |
Query PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
      PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
Sbjct PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
           |         |         |         |         |         |         |
           1        10        20        30        40        50        60
```

☑ **1SQM**   **STRUCTURE OF [R563A] LEUKOTRIENE A4 HYDROLASE**

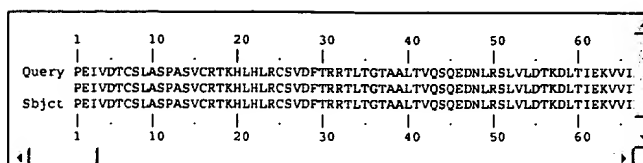|	
Chains	A
E Value	0.0
Characteristics	Deposited: 19-Mar-2004 Exp. Method: X Ray Diffraction Resolution: 2.30 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Leukotriene a 4 Hydrolase Mutation: R563A
Authors	Rudberg, P.C., Tholander, F.O.T., Andberg, M., Thunnissen, M.M.G.M.
Alignment stats	Length: 610 Score: 1220.68bits (3157) E-value: 0.0 Identities: 609/610 (100%) Positives: 609/61 (100%) Gaps: 0/610 (0%)

Alignment

```
        1      10       20       30       40       50       60
        |       |        |        |        |        |        |
Query  PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
       PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
Sbjct  PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVI
        |       |        |        |        |        |        |
        1      10       20       30       40       50       60
```

☑ **1Z1W**

Crystal structures of the tricorn interacting facor F3 from Thermoplasma acidophilum, a zinc aminopeptidase in three different conformations

Chains	A
E Value	4.07144E-20
Characteristics	Deposited: 07-Mar-2005 Exp. Method: X Ray Diffraction Resolution: 2.70 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Tricorn Protease Interacting Factor F3
Authors	Kyrieleis, O.J.P., Goettig, P., Kiefersauer, R., Huber, R., Brandstetter, H.
Alignment stats	Length: 426 Score: 95.9005bits (237) E-value: 4.07144E-20 Identities: 108/426 (25%) Positives: 177/426 (42%) Gaps: 57/426 (13%)

Alignment
```
         52     60     70       80       90      100     110
         |       |      |        |        |        |       |
Query : VLDTKDLTIEKVVNG  VEYALGEROSYKGSF LISLPIALSKI QEIVIEISF ISPASSALQW
        VLD    L I  -NG-- -     -Y G  -      A  -Q   IEISF      S
Sbjct  IVLDAVGLQINWYKVNG-I TA------IYDGOTVP-----AF I QF KIEISFAGEVSIS----
         |      |      |        |        |        |       |
         32     40     50       60       70       80
```

☑ **1Z5H**

Crystal structures of the Tricorn interacting Factor F3 from Thermoplasma acidophilum

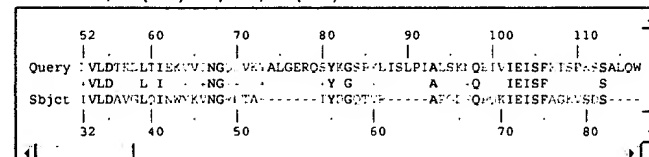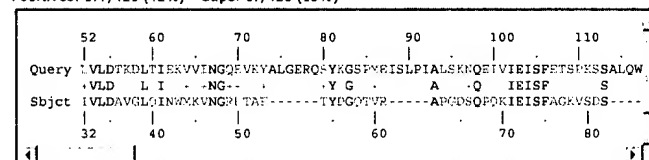|	
Chains	A,B
E Value	4.07144E-20
Characteristics	Deposited: 18-Mar-2005 Exp. Method: X Ray Diffraction Resolution: 2.30 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Tricorn Protease Interacting Factor F3
Authors	Kyrieleis, O.J.P., Goettig, P., Kiefersauer, R., Huber, R., Brandstetter, H.
Alignment stats	Length: 426 Score: 95.9005bits (237) E-value: 4.07144E-20 Identities: 108/426 (25%) Positives: 177/426 (42%) Gaps: 57/426 (13%)

Alignment
```
         52     60     70       80       90      100     110
         |       |      |        |        |        |       |
Query  LVLDTKDLTIEKVVINGQEVKYALGEROSYKGSPVEISLPIALSKNQEIVIEISFETSPKSSALQW
        VLD    L I  -NG-- -     -Y G  -      A  -Q   IEISF      S
Sbjct  IVLDAVGLQINWYKVNGPI TAF------TYPGOTVP-----APGDSQPQKIEISFAGEVSPS----
         |      |      |        |        |        |       |
         32     40     50       60       70       80
```

☑ **2GTQ**

Crystal structure of aminopeptidase N from human pathogen N. meningitides

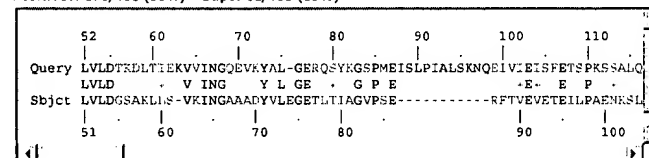|	
Chains	A
E Value	1.35851E-7
Characteristics	Deposited: 28-Apr-2006 Exp. Method: X Ray Diffraction Resolution: 2.05 Å
Classification	Hydrolase
Compound	Mol. Id: 1 Molecule: Aminopeptidase N
Authors	Nocek, B., Muligan, R., Bargassa, M., Joachimiak, A.
Alignment stats	Length: 481 Score: 54.299bits (129) E-value: 1.35851E-7 Identities: 111/481 (23%) Positives: 170/481 (35%) Gaps: 61/481 (13%)

Alignment
```
         52     60     70       80       90      100     110
         |       |      |        |        |        |       |
Query  LVLDTKDLTIEKVVINGQEVKYAL-GEROSYKGSPMEISLPIALSKNQEIVIEISFETSPKSSALQ
        LVLD   + V ING    Y L GE - G P E           -E- E P -
Sbjct  LVLDGSAKLIS-VKINGAAADYVLEGETLTIAGVPSE----------RFTVEVETEILPAENKSL
         |      |      |        |        |        |       |
         51     60     70       80                90      100
```

☑ **1NNJ**

Crystal structure Complex between the Lactococcus lactis Fpg and an abasic site containing DNA

Chains	A
E Value	2.10075
Characteristics	Deposited: 14-Jan-2003 Exp. Method: X Ray Diffraction Resolution: 1.90 Å
Classification	Hydrolase
Compound	Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase Mutation: P1G
Authors	Serre, L., Pereira de Jesus, K., Boiteux, S., Zelwer, C., Castaing, B.
Alignment stats	Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

Alignment

```
        281        290       300       310       320              330        3
         |    .     |    .    |    .    |    .    |    .     |     |      .    |
Query  TL AGDKSLSN.IAHEISHSWIGN VTNKIV  HWI ECHI  .------L. FICG LFGFH R
         TL·AG   L N·   E·   W  ·   K    .   H      L·· I  ·L G   R ·
Sbjct  TL·AG---LGN YVJE.I--WLA.IFEKI.J.IE-.IH. .DSIIELJ·AI--·L GS.IR:.
         |.          |    .   |    .    |    .    |    .     |      .    |
         164        170       180       190       200             210        220
```

☑ **1PJI**   Crystal structure of wild type Lactococcus lactis FPG complexed to a 1,3 propanediol containing DNA

Chains	A
E Value	2.10075
Characteristics	Deposited: 03-Jun-2003 Exp. Method: X Ray Diffraction
	Resolution: 1.90 Å
Classification	Hydrolase/dna
Compound	Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase
Authors	Pereira, K., Serre, L., Zelwer, C., Castaing, B.
Alignment stats	Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

Alignment

```
        281        290       300       310       320              330        3
         |    .     |    .    |    .    |    .    |    .     |     |      .    |
Query  TLLAGDKSLSNVIAHEISHSWIGNIVTNKTWDHFWLNEGHT VY------LERHICGRLFGERFRHF
         TL·AG   L N·   E·   W      K   ·   H ·+   L·· I  ·L G   R ·
Sbjct  TLVAG---LGNIYVDEVL--WLAK.HPEKETNQLIE·SIHLIFDSIIEIL.·AI--·KLGGSSIRTY
         |.          |    .   |    .    |    .    |    .     |      .    |
         164        170       180       190       200             210        220
```

☑ **1PJJ**   Complex between the Lactococcus lactis Fpg and an abasic site containing DNA.

Chains	A
E Value	2.10075
Characteristics	Deposited: 03-Jun-2003 Exp. Method: X Ray Diffraction
	Resolution: 1.90 Å
Classification	Hydrolase/dna
Compound	Mol. Id: 3 Molecule: Formamidopyrimidine DNA Glycosylase Mutation: P1G
Authors	Serre, L., Pereira de Jesus, K., Boiteux, S., Zelwer, C., Castaing, B.
Alignment stats	Length: 85 Score: 30.4166bits (67) E-value: 2.10075 Identities: 23/85 (27%) Positives: 42/85 (49%) Gaps: 13/85 (15%)

Alignment

```
        281        290       300       310       320              330        3
         |    .     |    .    |    .    |    .    |    .     |     |      .    |
Query  TLLAGDKSLSNVIAHEISHSWTGNLVTNKTWDHFWLNEGHTVY------LERHICGRLFGERFRHF
         TL·AG   L N·   E·   W   ·   K   ·   · H ·+   L·· I  ·L G   R +·
Sbjct  TLVAG---LGNIYVDEVL--WLAKIHPEKETNQLIESSIHLLHDSIIEILQKAI--KLGGSSIRTY
         |.          |    .   |    .    |    .    |    .     |      .    |
         164        170       180       190       200             210        220
```

1 2 ⇨

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:50:03 ; Search time 189 Seconds
                                      (without alignments)
                                 1418.101 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH..........HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                1: geneseqp1980s:*
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                7: geneseqp2003bs:*
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                9: geneseqp2005s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description
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     1   3225   100.0   611 3   AAB08840   Aab08840 Amino aci
     2   3225   100.0   611 8   ABM81460   Abm81460 Tumour-as
     3   3225   100.0   611 9   ADW07254   Adw07254 Human hep
     4   3225   100.0   611 9   ADZ04287   Adz04287 Human leu
     5   3222   99.9   611 7   ADE25724   Ade25724 Human pro
     6   3042.5 94.3   610 8   ADT66633   Adt66633 Rat leuko
     7   2963   91.9   625 3   AAB58111   Aab58111 Lung canc
     8   2696   83.6   532 8   ADL99491   Adl99491 Human leu

9	2438.5	75.6	480	8	ADL99494	Adl99494 Human leu
10	1464	45.4	587	8	ADN23312	Adn23312 Bacterial
11	1376.5	42.7	809	8	ADN23545	Adn23545 Bacterial
12	1338	41.5	613	4	ABB71965	Abb71965 Drosophil
13	1206.5	37.4	612	8	ADS44280	Ads44280 Bacterial
14	1134.5	35.2	671	6	ABR52866	Abr52866 Protein s
15	1134.5	35.2	671	7	ADK62338	Adk62338 Disease t
16	1134.5	35.2	671	8	ADN19334	Adn19334 Bacterial
17	1079	33.5	694	8	ADN21345	Adn21345 Bacterial
18	1059.5	32.9	623	2	AAW02284	Aaw02284 Candida a
19	1030.5	32.0	573	8	ADS30208	Ads30208 Bacterial
20	1018.5	31.6	584	9	ABM96671	Abm96671 M. xanthu
21	1006.5	31.2	650	5	AAU72906	Aau72906 Human met
22	1006.5	31.2	650	5	ADR43717	Adr43717 Human pro
23	1006.5	31.2	650	6	ABP59205	Abp59205 Human ami
24	1006.5	31.2	650	7	ADD45336	Add45336 Human Pro
25	1006.5	31.2	650	8	ABM80228	Abm80228 Tumour-as
26	1006.5	31.2	658	7	ADC31289	Adc31289 Human nov
27	1005.5	31.2	650	4	AAB84214	Aab84214 Amino aci
28	1001.5	31.1	650	7	ADD45334	Add45334 Rat Prote
29	1000	31.0	657	8	ADR97314	Adr97314 Human RNP
30	987	30.6	626	7	ADM05614	Adm05614 Human pro
31	954	29.6	569	8	ADN26507	Adn26507 Bacterial
32	947	29.4	671	8	ADS28564	Ads28564 Bacterial
33	929.5	28.8	588	8	ADS27297	Ads27297 Bacterial
34	929.5	28.8	588	8	ADS26935	Ads26935 Bacterial
35	929.5	28.8	641	8	ADS26559	Ads26559 Bacterial
36	887.5	27.5	650	8	ADY05243	Ady05243 Plant ful
37	880	27.3	540	8	ADN26764	Adn26764 Bacterial
38	874	27.1	581	8	ADS28769	Ads28769 Bacterial
39	800.5	24.8	724	5	AAU72907	Aau72907 Human met
40	800	24.8	725	5	ABB77908	Abb77908 Amino aci
41	800	24.8	725	8	ADL14157	Adl14157 Novel hum
42	766.5	23.8	416	4	AAM25679	Aam25679 Human pro
43	721	22.4	541	5	ADR41508	Adr41508 Human CD-
44	715.5	22.2	756	8	ADJ67633	Adj67633 Human ova
45	671.5	20.8	501	8	ADJ71950	Adj71950 Human PMM

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:03:01 ; Search time 47 Seconds
                                              (without alignments)
                                              1073.025 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH..........HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1059.5	32.9	623	1	US-08-332-838-2	Sequence 2, Appli
3	1018.5	31.6	584	2	US-09-902-540-15870	Sequence 15870, A
4	1006.5	31.2	650	2	US-10-363-937-5	Sequence 5, Appli
5	1005.5	31.2	650	2	US-09-443-795-1	Sequence 1, Appli
6	840.5	26.1	362	2	US-09-270-767-43340	Sequence 43340, A
7	785.5	24.4	587	2	US-09-949-016-9933	Sequence 9933, Ap
8	783	24.3	429	2	US-09-248-796A-17980	Sequence 17980, A
9	557.5	17.3	285	2	US-09-270-767-42260	Sequence 42260, A
10	341	10.6	972	2	US-08-335-844A-23	Sequence 23, Appl
11	341	10.6	972	2	US-09-129-366-23	Sequence 23, Appl

12	340.5	10.6	1025	1	US-08-530-792D-23	Sequence 23, Appl
13	337	10.4	972	2	US-08-335-844A-24	Sequence 24, Appl
14	337	10.4	972	2	US-09-129-366-24	Sequence 24, Appl
15	330	10.2	1026	1	US-08-530-792D-22	Sequence 22, Appl
16	328	10.2	923	2	US-09-328-352-4371	Sequence 4371, Ap
17	324	10.0	919	2	US-09-919-039-222	Sequence 222, App
18	311	9.6	354	2	US-09-949-016-6929	Sequence 6929, Ap
19	304.5	9.4	990	2	US-10-363-937-7	Sequence 7, Appli
20	304	9.4	977	2	US-08-335-844A-22	Sequence 22, Appl
21	304	9.4	977	2	US-09-129-366-22	Sequence 22, Appl
22	298.5	9.3	957	2	US-09-949-016-6154	Sequence 6154, Ap
23	298.5	9.3	964	2	US-09-949-016-7431	Sequence 7431, Ap
24	298.5	9.3	967	2	US-09-139-802-201	Sequence 201, App
25	298.5	9.3	967	2	US-09-659-786-201	Sequence 201, App
26	297	9.2	850	2	US-09-902-540-10199	Sequence 10199, A
27	297	9.2	867	2	US-09-540-236-3193	Sequence 3193, Ap
28	296.5	9.2	699	2	US-09-270-767-45507	Sequence 45507, A
29	291.5	9.0	848	2	US-09-583-110-2738	Sequence 2738, Ap
30	290.5	9.0	912	2	US-09-902-540-16181	Sequence 16181, A
31	285	8.8	948	2	US-09-620-312D-1105	Sequence 1105, Ap
32	284	8.8	917	2	US-09-902-540-12845	Sequence 12845, A
33	281.5	8.7	941	2	US-09-991-181-353	Sequence 353, App
34	281.5	8.7	941	2	US-09-990-444-353	Sequence 353, App
35	281.5	8.7	941	2	US-09-997-333-353	Sequence 353, App
36	281.5	8.7	941	2	US-09-992-598-353	Sequence 353, App
37	273	8.5	874	2	US-09-489-039A-12124	Sequence 12124, A
38	264.5	8.2	815	2	US-09-107-433-5059	Sequence 5059, Ap
39	259.5	8.0	458	2	US-09-602-777A-124	Sequence 124, App
40	258	8.0	896	2	US-09-543-681A-7870	Sequence 7870, Ap
41	245.5	7.6	867	2	US-09-602-777A-104	Sequence 104, App
42	245	7.6	990	2	US-09-657-931A-11	Sequence 11, Appl
43	244.5	7.6	891	2	US-09-252-991A-28689	Sequence 28689, A
44	244.5	7.6	986	2	US-09-657-931A-12	Sequence 12, Appl
45	242	7.5	995	2	US-09-657-931A-1	Sequence 1, Appli

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:11:02 ; Search time 166 Seconds
                                               (without alignments)
                                      1535.397 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.........HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
        1   3225 100.0   611   5   US-10-873-595-6   Sequence 6, Appli
        2   3222   99.9   611   4   US-10-247-671-128   Sequence 128, App
        3   2963   91.9   625   3   US-09-925-302-449   Sequence 449, App
        4   2963   91.9   625   3   US-09-925-302-449   Sequence 449, App
        5   1464   45.4   587   4   US-10-369-493-5965   Sequence 5965, Ap
   ·   6 1376.5   42.7   809   4   US-10-369-493-6198   Sequence 6198, Ap
        7   1338   41.5   613   6   US-11-097-143-42687   Sequence 42687, A
        8 1206.5   37.4   612   4   US-10-369-493-22710   Sequence 22710, A
        9 1134.5   35.2   671   4   US-10-369-493-1987   Sequence 1987, Ap
       10   1079   33.5   694   4   US-10-369-493-3998   Sequence 3998, Ap
       11 1030.5   32.0   573   4   US-10-369-493-19241   Sequence 19241, A

12	1006.5	31.2	650	4	US-10-363-937-5	Sequence 5, Appli
13	1006.5	31.2	650	4	US-10-275-107-66	Sequence 66, Appl
14	1006.5	31.2	650	6	US-11-167-040-5	Sequence 5, Appli
15	1005.5	31.2	650	3	US-09-854-875A-1	Sequence 1, Appli
16	1005.5	31.2	650	4	US-10-056-253-1	Sequence 1, Appli
17	1005.5	31.2	650	5	US-10-767-308-1	Sequence 1, Appli
18	987	30.6	626	4	US-10-108-260A-4299	Sequence 4299, Ap
19	954	29.6	569	4	US-10-369-493-9160	Sequence 9160, Ap
20	947	29.4	671	4	US-10-369-493-17597	Sequence 17597, A
21	929.5	28.8	588	4	US-10-369-493-15968	Sequence 15968, A
22	929.5	28.8	588	4	US-10-369-493-16330	Sequence 16330, A
23	929.5	28.8	641	4	US-10-369-493-15592	Sequence 15592, A
24	892.5	27.7	611	4	US-10-425-115-272788	Sequence 272788,
25	887.5	27.5	650	4	US-10-425-114-61058	Sequence 61058, A
26	880.5	27.3	611	4	US-10-437-963-143613	Sequence 143613,
27	880	27.3	540	4	US-10-369-493-9417	Sequence 9417, Ap
28	874	27.1	581	4	US-10-369-493-17802	Sequence 17802, A
29	800.5	24.8	724	4	US-10-275-107-67	Sequence 67, Appl
30	800	24.8	725	3	US-09-929-218-2	Sequence 2, Appli
31	800	24.8	725	4	US-10-423-543-40	Sequence 40, Appl
32	766.5	23.8	416	4	US-10-296-115-1194	Sequence 1194, Ap
33	593	18.4	363	4	US-10-767-701-42438	Sequence 42438, A
34	534	16.6	358	4	US-10-424-599-157271	Sequence 157271,
35	517	16.0	416	4	US-10-311-035-3	Sequence 3, Appli
36	401	12.4	393	4	US-10-099-322-301	Sequence 301, App
37	401	12.4	393	4	US-10-044-564-301	Sequence 301, App
38	365.5	11.3	821	4	US-10-369-493-19382	Sequence 19382, A
39	362	11.2	441	4	US-10-007-271-4	Sequence 4, Appli
40	353.5	11.0	875	4	US-10-369-493-20117	Sequence 20117, A
41	347.5	10.8	438	4	US-10-281-904-4	Sequence 4, Appli
42	345.5	10.7	799	4	US-10-425-115-205689	Sequence 205689,
43	344	10.7	694	4	US-10-087-192-1851	Sequence 1851, Ap
44	343	10.6	723	4	US-10-369-493-10942	Sequence 10942, A
45	342	10.6	1025	4	US-10-087-192-1854	Sequence 1854, Ap

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OM protein - protein search, using sw model

Run on: November 25, 2005, 19:02:46 ; Search time 5 Seconds
                                    (without alignments)
                                    369.778 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH..........HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
                 1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	342	10.6	1092	1	US-10-821-234-999	Sequence 999, App
2	281.5	8.7	941	1	US-10-131-826A-464	Sequence 464, App
3	252.5	7.8	1024	1	US-10-131-826A-198	Sequence 198, App
4	93	2.9	2323	1	US-10-793-626-760	Sequence 760, App
5	91.5	2.8	406	1	US-10-131-826A-502	Sequence 502, App
6	87	2.7	903	7	US-11-057-058-65	Sequence 65, Appl
7	86.5	2.7	314	1	US-10-793-626-2552	Sequence 2552, Ap
8	85	2.6	434	1	US-10-821-234-1553	Sequence 1553, Ap
9	85	2.6	871	7	US-11-077-550-2	Sequence 2, Appli

10	85	2.6	871	7	US-11-077-550-8	Sequence 8, Appli
11	85	2.6	871	7	US-11-077-550-26	Sequence 26, Appl
12	85	2.6	871	7	US-11-077-550-153	Sequence 153, App
13	85	2.6	873	7	US-11-077-550-6	Sequence 6, Appli
14	85	2.6	873	7	US-11-077-550-149	Sequence 149, App
15	85	2.6	873	7	US-11-077-550-151	Sequence 151, App
16	85	2.6	879	7	US-11-077-550-159	Sequence 159, App
17	85	2.6	894	7	US-11-077-550-4	Sequence 4, Appli
18	85	2.6	1127	7	US-11-077-550-40	Sequence 40, Appl
19	85	2.6	1129	7	US-11-077-550-42	Sequence 42, Appl
20	84.5	2.6	944	7	US-11-057-058-68	Sequence 68, Appl
21	84	2.6	556	1	US-10-821-234-1509	Sequence 1509, Ap
22	84	2.6	3056	7	US-11-109-156-20	Sequence 20, Appl
23	83.5	2.6	1130	7	US-11-077-550-139	Sequence 139, App
24	83	2.6	966	7	US-11-057-058-67	Sequence 67, Appl
25	82.5	2.6	775	1	US-10-131-826A-120	Sequence 120, App
26	82.5	2.6	2080	1	US-10-821-234-1640	Sequence 1640, Ap
27	82	2.5	873	7	US-11-077-550-167	Sequence 167, App
28	82	2.5	875	7	US-11-077-550-10	Sequence 10, Appl
29	81.5	2.5	423	7	US-11-184-156-2	Sequence 2, Appli
30	81	2.5	877	7	US-11-077-550-157	Sequence 157, App
31	80	2.5	485	1	US-10-630-203-2	Sequence 2, Appli
32	80	2.5	485	7	US-11-103-037-1	Sequence 1, Appli
33	80	2.5	532	1	US-10-821-234-918	Sequence 918, App
34	80	2.5	1304	1	US-10-821-234-1648	Sequence 1648, Ap
35	79.5	2.5	138	1	US-10-793-626-1540	Sequence 1540, Ap
36	79.5	2.5	176	1	US-10-793-626-612	Sequence 612, App
37	79.5	2.5	878	7	US-11-077-550-12	Sequence 12, Appl
38	79.5	2.5	887	7	US-11-077-550-161	Sequence 161, App
39	79.5	2.5	907	7	US-11-077-550-16	Sequence 16, Appl
40	79.5	2.5	953	7	US-11-077-550-14	Sequence 14, Appl
41	79.5	2.5	1013	7	US-11-077-550-18	Sequence 18, Appl
42	79.5	2.5	1432	1	US-10-510-386-218	Sequence 218, App
43	79	2.4	468	7	US-11-054-385-12	Sequence 12, Appl
44	79	2.4	871	7	US-11-077-550-155	Sequence 155, App
45	79	2.4	873	7	US-11-077-550-163	Sequence 163, App

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:59:55 ; Search time 42 Seconds
                                             (without alignments)
                                 1397.434 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH.........HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
      1   3225   100.0   611 1   S65947   leukotriene-A4 hyd
      2   3058   94.8   611 1   JN0066   leukotriene-A4 hyd
      3   3043   94.4   611 1   JC4237   leukotriene-A4 hyd
      4 3042.5   94.3   610 1   S20444   leukotriene-A4 hyd
      5   1464   45.4   587 2   T32546   hypothetical prote
      6 1376.5   42.7   809 2   T32899   probable leukotrie
      7 1206.5   37.4   612 2   T40936   probable leukotrie
      8 1134.5   35.2   671 2   S61099   leukotriene-A4 hyd
      9   947   29.4   671 2   D82675   aminopeptidase N X
     10   668   20.7   360 2   T51870   hypothetical prote
     11   388.5   12.0   785 2   S73098   aminopeptidase (EC
     12   354.5   11.0   844 2   JC4054   membrane alanyl am
     13   344.5   10.7   844 2   S47274   membrane alanyl am

14	341	10.6	1006	2	A59384	oxytocinase/insuli
15	341	10.6	1025	2	A59383	oxytocinase/insuli
16	340.5	10.6	916	2	I55441	vp165 - rat
17	337.5	10.5	843	2	S38364	membrane alanyl am
18	324.5	10.1	784	2	B90442	tricorn proteinase
19	317	9.8	920	2	T10052	aminopeptidase (EC
20	313.5	9.7	866	2	AI1880	aminopeptidase [im
21	310.5	9.6	988	2	T24668	hypothetical prote
22	308	9.6	964	2	G96662	probable aminopept
23	307	9.5	780	2	T37456	Tricorn proteinase
24	305.5	9.5	869	2	S76720	hypothetical prote
25	302	9.4	849	2	JC7959	lysyl aminopeptida
26	301.5	9.3	884	2	T29637	hypothetical prote
27	300	9.3	849	2	JU0191	aminopeptidase Y (
28	298.5	9.3	957	2	A47531	glutamyl aminopept
29	298.5	9.3	967	2	A30325	membrane alanyl am
30	297	9.2	472	2	A75464	probable zinc meta
31	296.5	9.2	990	2	JC8058	laeverin - human
32	291.5	9.0	848	2	B97960	membrane alanyl am
33	290.5	9.0	848	2	E95092	aminopeptidase N [
34	289	9.0	747	2	T23882	hypothetical prote
35	285	8.8	805	2	S07099	membrane alanyl am
36	284.5	8.8	882	2	T39789	aminopeptidase - f
37	281	8.7	862	2	G87094	probable aminopept
38	281	8.7	963	2	A53984	membrane alanyl am
39	279	8.7	965	2	A32852	membrane alanyl am
40	277	8.6	861	2	B70866	probable aminopept
41	275.5	8.5	844	2	S37794	aminopeptidase ysc
42	274.5	8.5	945	2	S30398	aminopeptidase N h
43	274	8.5	786	2	T23883	hypothetical prote
44	274	8.5	919	2	S42842	T16G12.2 protein -
45	273	8.5	783	2	T37457	Tricorn proteinase

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OM protein - protein search, using sw model

Run on: November 25, 2005, 18:59:39 ; Search time 231 Seconds
                                            (without alignments)
                                            1863.083 Million cell updates/sec

Title: US-09-914-451-1
Perfect score: 3225
Sequence: 1 PEIVDTCSLASPASVCRTKH..........HKASMHPVTAMLVGKDLKVD 610

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     1   3225   100.0   610 1   LKHA4_HUMAN   P09960 homo sapien
     2   3225   100.0   611 2   Q6IAT6_HUMAN   Q6iat6 homo sapien
     3   3202   99.3   611 2   Q5REQ3_PONPY   Q5req3 pongo pygma
     4   3090   95.8   610 1   LKHA4_CHILA   Q6s9c8 chinchilla
     5   3061   94.9   610 1   LKHA4_MOUSE   P24527 mus musculu
     6   3043   94.4   610 1   LKHA4_CAVPO   P19602 cavia porce
     7   3042.5   94.3   609 1   LKHA4_RAT   P30349 rattus norv
     8   2540.5   78.8   612 2   Q5ZJJ6_CHICK   Q5zjj6 gallus gall
     9   2294.5   71.1   609 2   Q6IP81_XENLA   Q6ip81 xenopus lae
    10   2284.5   70.8   609 2   Q6GL78_XENTR   Q6gl78 xenopus tro
    11   2190.5   67.9   611 2   Q5RIF1_BRARE   Q5rif1 brachydanio
    12   2180.5   67.6   611 2   Q6NUX4_BRARE   Q6nux4 brachydanio
    13   2077.5   64.4   630 2   Q4T8V9_TETNG   Q4t8v9 tetraodon n
    14   1487   46.1   625 2   O44183_CAEEL   O44183 caenorhabdi
    15   1480   45.9   625 2   Q61MW9_CAEBR   Q61mw9 caenorhabdi

16	1386.5	43.0	558	2	Q7Q192_ANOGA	Q7q192	anopheles g
17	1376.5	42.7	609	2	O44969_CAEEL	O44969	caenorhabdi
18	1369	42.4	608	2	Q86GU4_CAEEL	Q86gu4	caenorhabdi
19	1338	41.5	613	2	Q7KT44_DROME	Q7kt44	drosophila
20	1338	41.5	684	2	Q9VJ39_DROME	Q9vj39	drosophila
21	1315	40.8	606	2	Q55BR5_DICDI	Q55br5	dictyosteli
22	1212.5	37.6	614	2	Q4X265_ASPFU	Q4x265	aspergillus
23	1206.5	37.4	612	1	LKHA4_SCHPO	O94544	schizosacch
24	1199.5	37.2	647	2	Q6C3E5_YARLI	Q6c3e5	yarrowia li
25	1196.5	37.1	639	2	Q4HXX0_GIBZE	Q4hxx0	gibberella
26	1149.5	35.6	662	2	Q6CLD3_KLULA	Q6cld3	kluyveromyc
27	1145.5	35.5	652	2	Q6FTM0_CANGA	Q6ftm0	candida gla
28	1144.5	35.5	639	2	Q5B0W8_EMENI	Q5b0w8	aspergillus
29	1141	35.4	614	2	Q7S785_NEUCR	Q7s785	neurospora
30	1136	35.2	1297	2	Q4PI93_USTMA	Q4pi93	ustilago ma
31	1134.5	35.2	671	1	LKHA4_YEAST	Q10740	saccharomyc
32	1126	34.9	613	2	Q51X77_MAGGR	Q51x77	magnaporthe
33	1110	34.4	632	2	Q55RS1_CRYNE	Q55rs1	cryptococcu
34	1097.5	34.0	641	2	Q6BW21_DEBHA	Q6bw21	debaryomyce
35	1090	33.8	626	2	Q6DGD8_BRARE	Q6dgd8	brachydanio
36	1084	33.6	219	2	Q59ES1_HUMAN	Q59es1	homo sapien
37	1060.5	32.9	623	2	Q59NB8_CANAL	Q59nb8	candida alb
38	1026.5	31.8	618	2	Q6NVR0_XENTR	Q6nvr0	xenopus tro
39	1018.5	31.6	618	2	Q6GQ32_XENLA	Q6gq32	xenopus lae
40	1016.5	31.5	612	2	Q641C7_XENLA	Q641c7	xenopus lae
41	1014	31.4	650	1	AMPB_MOUSE	Q8vct3	mus musculu
42	1008.5	31.3	658	2	Q7RU04_HUMAN	Q7ru04	homo sapien
43	1006.5	31.2	650	1	AMPB_HUMAN	Q9h4a4	homo sapien
44	1005.5	31.2	286	2	Q5TZ09_BRARE	Q5tz09	brachydanio
45	1001.5	31.1	650	1	AMPB_RAT	O09175	rattus norv